

Run on: December 13, 2004, 21:48:04 ; Search time 27.5 Seconds
(without alignments)
935.687 Million cell updates/sec

Title: US-09-423-018-8
Perfect score: 2119
Sequence: 1 MGRGLLRGLWPLHLVLWTRI.....MHEALHNHYTQKSLSLSPGK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Issued_Patents_AA:*
1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
score greater than or equal to the score of the result being printed,
and is derived by analysis of the total score distribution.

SUMMARIES

Result	Score	% Query Match	Length	DB	ID	Description
1	1259.5	59.4	376	3	US-09-180-100-22	Sequence 22, Appl
2	1258	59.4	911	2	US-08-484-438-10	Sequence 10, Appl
3	1255.5	59.2	424	3	US-09-333-593A-8	Sequence 8, Appli
4	1254.5	59.2	360	3	US-09-180-100-11	Sequence 11, Appl
5	1253	59.1	388	3	US-09-131-247-16	Sequence 16, Appl
6	1253	59.1	388	4	US-09-784-623-16	Sequence 16, Appl
7	1253	59.1	398	4	US-09-612-033B-14	Sequence 14, Appl
8	1253	59.1	592	4	US-09-313-942-8	Sequence 8, Appli
9	1252	59.1	977	4	US-09-590-656-1	Sequence 1, Appli
10	1252	59.1	977	4	US-09-733-764-1	Sequence 1, Appli
11	1251.5	59.1	497	4	US-09-499-846-6	Sequence 6, Appli
12	1251.5	59.1	525	4	US-09-499-846-4	Sequence 4, Appli
13	1250.5	59.0	347	1	US-07-940-861-43	Sequence 43, Appl
14	1250.5	59.0	347	1	US-08-459-512-43	Sequence 43, Appl
15	1250.5	59.0	347	2	US-08-459-657-43	Sequence 43, Appl
16	1250.5	59.0	347	2	US-08-460-132-43	Sequence 43, Appl
17	1250.5	59.0	347	3	US-08-466-465-8	Sequence 8, Appli
18	1250.5	59.0	347	4	US-09-730-465-8	Sequence 8, Appli

19	1250.5	59.0	347	5	PCT-US92-02050-43	Sequence 43, Appl
20	1246	58.8	387	1	US-08-470-299-4	Sequence 4, Appli
21	1243.5	58.7	664	3	US-08-957-063-18	Sequence 18, Appl
22	1243.5	58.7	664	3	US-09-487-685-18	Sequence 18, Appl
23	1243.5	58.7	664	3	US-08-802-805D-18	Sequence 18, Appl
24	1243.5	58.7	664	4	US-09-388-316C-18	Sequence 18, Appl
25	1243	58.7	283	4	US-09-854-864-9	Sequence 9, Appli
26	1243	58.7	691	4	US-09-313-942-20	Sequence 20, Appl
27	1243	58.7	694	4	US-09-313-942-22	Sequence 22, Appl
28	1241	58.6	482	3	US-09-189-129-2	Sequence 2, Appli
29	1241	58.6	482	4	US-09-824-286-2	Sequence 2, Appli
30	1240	58.5	331	3	US-09-178-869-2	Sequence 2, Appli
31	1240	58.5	331	4	US-09-761-413-2	Sequence 2, Appli
32	1240	58.5	859	4	US-09-313-942-7	Sequence 7, Appli
33	1239.5	58.5	475	4	US-09-740-002-27	Sequence 27, Appl
34	1239.5	58.5	476	3	US-08-487-550-4	Sequence 4, Appli
35	1239.5	58.5	476	3	US-08-487-550-12	Sequence 12, Appl
36	1239.5	58.5	476	4	US-09-526-098-4	Sequence 4, Appli
37	1239.5	58.5	476	4	US-09-526-098-12	Sequence 12, Appl
38	1239.5	58.5	476	4	US-09-383-916-4	Sequence 4, Appli
39	1239.5	58.5	476	4	US-09-383-916-12	Sequence 12, Appl
40	1239.5	58.5	478	3	US-08-487-550-8	Sequence 8, Appli
41	1239.5	58.5	478	4	US-09-526-098-8	Sequence 8, Appli
42	1239.5	58.5	478	4	US-09-383-916-8	Sequence 8, Appli
43	1239.5	58.5	784	4	US-09-313-942-30	Sequence 30, Appl
44	1239	58.5	680	3	US-08-227-496C-15	Sequence 15, Appl
45	1238.5	58.4	371	1	US-08-236-311-7	Sequence 7, Appli

Run on: December 13, 2004, 21:57:06 ; Search time 101 Seconds
 (without alignments)
 1372.131 Million cell updates/sec

Title: US-09-423-018-8
 Perfect score: 2119
 Sequence: 1 MGRGLLRGLWPLHLVLWTRI.....MHEALHNHYTQKSLSLSPGK 388

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
- 17: /cgn2_6/ptodata/2/pubpaa/US10_NEW_PUB.pep:*
- 18: /cgn2_6/ptodata/2/pubpaa/US11_NEW_PUB.pep:*
- 19: /cgn2_6/ptodata/2/pubpaa/US60_NEW_PUB.pep:*
- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

		%					
Result		Query					
No.	Score	Match	Length	DB	ID	Description	
1	2119	100.0	388	9	US-09-734-300-8	Sequence 8, Appli	
2	2042	96.4	388	9	US-09-734-300-9	Sequence 9, Appli	
3	1278.5	60.3	396	14	US-10-193-616-14	Sequence 14, Appl	
4	1270.5	60.0	360	14	US-10-390-566-20	Sequence 20, Appl	

5	1270.5	60.0	360	14	US-10-390-566-27	Sequence 27, Appl
6	1270.5	60.0	367	14	US-10-390-566-19	Sequence 19, Appl
7	1270.5	60.0	367	14	US-10-390-566-26	Sequence 26, Appl
8	1269.5	59.9	360	14	US-10-390-566-7	Sequence 7, Appli
9	1269.5	59.9	360	14	US-10-390-566-14	Sequence 14, Appl
10	1269.5	59.9	367	14	US-10-390-566-6	Sequence 6, Appli
11	1269.5	59.9	367	14	US-10-390-566-13	Sequence 13, Appl
12	1269	59.9	608	14	US-10-363-427-10	Sequence 10, Appl
13	1263	59.6	366	15	US-10-258-368-6	Sequence 6, Appli
14	1262	59.6	334	15	US-10-258-368-8	Sequence 8, Appli
15	1261	59.5	444	14	US-10-363-427-2	Sequence 2, Appli
16	1261	59.5	628	14	US-10-363-427-6	Sequence 6, Appli
17	1259.5	59.4	376	9	US-09-949-713-22	Sequence 22, Appl
18	1259.5	59.4	376	14	US-10-084-139-10	Sequence 10, Appl
19	1259.5	59.4	450	17	US-10-768-932A-2	Sequence 2, Appli
20	1256.5	59.3	1367	17	US-10-473-127-281	Sequence 281, App
21	1255	59.2	443	14	US-10-151-071-5	Sequence 5, Appli
22	1255	59.2	443	14	US-10-166-232A-5	Sequence 5, Appli
23	1255	59.2	634	16	US-10-416-011-2	Sequence 2, Appli
24	1254.5	59.2	360	9	US-09-949-713-11	Sequence 11, Appl
25	1253	59.1	388	9	US-09-784-623-16	Sequence 16, Appl
26	1253	59.1	388	17	US-10-748-112-3	Sequence 3, Appli
27	1253	59.1	398	15	US-10-622-407-14	Sequence 14, Appl
28	1253	59.1	592	9	US-09-313-942-8	Sequence 8, Appli
29	1253	59.1	592	9	US-09-935-868-8	Sequence 8, Appli
30	1253	59.1	592	14	US-10-287-035-8	Sequence 8, Appli
31	1253	59.1	592	14	US-10-282-162-8	Sequence 8, Appli
32	1252.5	59.1	400	10	US-09-389-782-5	Sequence 5, Appli
33	1252	59.1	407	10	US-09-389-782-3	Sequence 3, Appli
34	1252	59.1	413	10	US-09-389-782-4	Sequence 4, Appli
35	1252	59.1	977	9	US-09-733-764-1	Sequence 1, Appli
36	1252	59.1	977	14	US-10-357-653-1	Sequence 1, Appli
37	1251.5	59.1	321	17	US-10-804-532-3	Sequence 3, Appli
38	1251.5	59.1	391	17	US-10-804-532-4	Sequence 4, Appli
39	1251.5	59.1	497	15	US-10-683-255-6	Sequence 6, Appli
40	1251.5	59.1	525	15	US-10-683-255-4	Sequence 4, Appli
41	1250.5	59.0	347	9	US-09-796-033-8	Sequence 8, Appli
42	1250.5	59.0	347	9	US-09-730-465-8	Sequence 8, Appli
43	1250.5	59.0	347	13	US-10-091-236-17	Sequence 17, Appl
44	1250.5	59.0	347	14	US-10-091-313-7	Sequence 7, Appli
45	1250.5	59.0	347	14	US-10-091-268-7	Sequence 7, Appli

Run on: December 13, 2004, 21:48:04 ; Search time 27.5 Seconds
 (without alignments)
 935.687 Million cell updates/sec

Title: US-09-423-018-9
 Perfect score: 2125
 Sequence: 1 MGRGLLRGLWPLHIVLWTRI.....MHEALHNHYTQKSLSLSPGK 388

Scoring table: BLOSUM62
 Gapop 10.0 , Gapext 0.5

Searched: 478139 seqs, 66318000 residues

Total number of hits satisfying chosen parameters: 478139

Minimum DB seq length: 0
 Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
 Maximum Match 100%
 Listing first 45 summaries

Database : Issued_Patents_AA:*
 1: /cgn2_6/ptodata/1/iaa/5A_COMB.pep:*
 2: /cgn2_6/ptodata/1/iaa/5B_COMB.pep:*
 3: /cgn2_6/ptodata/1/iaa/6A_COMB.pep:*
 4: /cgn2_6/ptodata/1/iaa/6B_COMB.pep:*
 5: /cgn2_6/ptodata/1/iaa/PCTUS_COMB.pep:*
 6: /cgn2_6/ptodata/1/iaa/backfiles1.pep:*

Pred. No. is the number of results predicted by chance to have a
 score greater than or equal to the score of the result being printed,
 and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	1265	59.5	398	4	US-09-612-033B-14	Sequence 14, Appl
2	1263	59.4	592	4	US-09-313-942-8	Sequence 8, Appli
3	1262.5	59.4	376	3	US-09-180-100-22	Sequence 22, Appl
4	1260	59.3	911	2	US-08-484-438-10	Sequence 10, Appl
5	1257.5	59.2	424	3	US-09-333-593A-8	Sequence 8, Appli
6	1257	59.2	360	3	US-09-180-100-11	Sequence 11, Appl
7	1256	59.1	397	4	US-09-854-864-18	Sequence 18, Appl
8	1252.5	58.9	784	4	US-09-313-942-30	Sequence 30, Appl
9	1252	58.9	388	3	US-09-131-247-16	Sequence 16, Appl
10	1252	58.9	388	4	US-09-784-623-16	Sequence 16, Appl
11	1251.5	58.9	347	1	US-07-940-861-43	Sequence 43, Appl
12	1251.5	58.9	347	1	US-08-459-512-43	Sequence 43, Appl
13	1251.5	58.9	347	2	US-08-459-657-43	Sequence 43, Appl
14	1251.5	58.9	347	2	US-08-460-132-43	Sequence 43, Appl
15	1251.5	58.9	347	3	US-08-466-465-8	Sequence 8, Appli
16	1251.5	58.9	347	4	US-09-730-465-8	Sequence 8, Appli
17	1251.5	58.9	347	5	PCT-US92-02050-43	Sequence 43, Appl
18	1250.5	58.8	437	5	PCT-US96-10043-11	Sequence 11, Appl

19	1247.5	58.7	497	4	US-09-499-846-6	Sequence 6, Appli
20	1247.5	58.7	525	4	US-09-499-846-4	Sequence 4, Appli
21	1247	58.7	387	1	US-08-470-299-4	Sequence 4, Appli
22	1247	58.7	977	4	US-09-590-656-1	Sequence 1, Appli
23	1247	58.7	977	4	US-09-733-764-1	Sequence 1, Appli
24	1244	58.5	631	4	US-09-056-461-22	Sequence 22, Appl
25	1242.5	58.5	664	3	US-08-957-063-16	Sequence 16, Appl
26	1242.5	58.5	664	3	US-09-487-685-16	Sequence 16, Appl
27	1242.5	58.5	664	3	US-08-802-805D-16	Sequence 16, Appl
28	1242.5	58.5	664	4	US-09-388-316C-16	Sequence 16, Appl
29	1242.5	58.5	704	4	US-09-590-656-2	Sequence 2, Appli
30	1242.5	58.5	704	4	US-09-733-764-2	Sequence 2, Appli
31	1241.5	58.4	475	4	US-09-740-002-27	Sequence 27, Appl
32	1241.5	58.4	476	3	US-08-487-550-4	Sequence 4, Appli
33	1241.5	58.4	476	3	US-08-487-550-12	Sequence 12, Appl
34	1241.5	58.4	476	4	US-09-526-098-4	Sequence 4, Appli
35	1241.5	58.4	476	4	US-09-526-098-12	Sequence 12, Appl
36	1241.5	58.4	476	4	US-09-383-916-4	Sequence 4, Appli
37	1241.5	58.4	476	4	US-09-383-916-12	Sequence 12, Appl
38	1241.5	58.4	478	3	US-08-487-550-8	Sequence 8, Appli
39	1241.5	58.4	478	4	US-09-526-098-8	Sequence 8, Appli
40	1241.5	58.4	478	4	US-09-383-916-8	Sequence 8, Appli
41	1241.5	58.4	482	3	US-09-189-129-2	Sequence 2, Appli
42	1241.5	58.4	482	4	US-09-824-286-2	Sequence 2, Appli
43	1241	58.4	680	3	US-08-227-496C-15	Sequence 15, Appl
44	1241	58.4	859	4	US-09-313-942-7	Sequence 7, Appli
45	1240.5	58.4	371	1	US-08-236-311-7	Sequence 7, Appli

Search completed: December 13, 2004, 22:00:36
Job time : 28.5 secs

GenCore version 5.1.6
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OM protein - protein search, using sw model

Run on: December 13, 2004, 21:57:06 ; Search time 101 Seconds
(without alignments)
1372.131 Million cell updates/sec

Title: US-09-423-018-9
Perfect score: 2125
Sequence: 1 MGRGLLRGLWPLHIVLWTRI.....MHEALHNHYTQKSLSLSPGK 388

Scoring table: BLOSUM62
Gapop 10.0 , Gapext 0.5

Searched: 1585576 seqs, 357178320 residues

Total number of hits satisfying chosen parameters: 1585576

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Maximum DB seq length: 2000000000

Post-processing: Minimum Match 0%
Maximum Match 100%
Listing first 45 summaries

Database : Published Applications_AA:*

- 1: /cgn2_6/ptodata/2/pubpaa/US07_PUBCOMB.pep:*
- 2: /cgn2_6/ptodata/2/pubpaa/PCT_NEW_PUB.pep:*
- 3: /cgn2_6/ptodata/2/pubpaa/US06_NEW_PUB.pep:*
- 4: /cgn2_6/ptodata/2/pubpaa/US06_PUBCOMB.pep:*
- 5: /cgn2_6/ptodata/2/pubpaa/US07_NEW_PUB.pep:*
- 6: /cgn2_6/ptodata/2/pubpaa/PCTUS_PUBCOMB.pep:*
- 7: /cgn2_6/ptodata/2/pubpaa/US08_NEW_PUB.pep:*
- 8: /cgn2_6/ptodata/2/pubpaa/US08_PUBCOMB.pep:*
- 9: /cgn2_6/ptodata/2/pubpaa/US09A_PUBCOMB.pep:*
- 10: /cgn2_6/ptodata/2/pubpaa/US09B_PUBCOMB.pep:*
- 11: /cgn2_6/ptodata/2/pubpaa/US09C_PUBCOMB.pep:*
- 12: /cgn2_6/ptodata/2/pubpaa/US09_NEW_PUB.pep:*
- 13: /cgn2_6/ptodata/2/pubpaa/US10A_PUBCOMB.pep:*
- 14: /cgn2_6/ptodata/2/pubpaa/US10B_PUBCOMB.pep:*
- 15: /cgn2_6/ptodata/2/pubpaa/US10C_PUBCOMB.pep:*
- 16: /cgn2_6/ptodata/2/pubpaa/US10D_PUBCOMB.pep:*
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- 20: /cgn2_6/ptodata/2/pubpaa/US60_PUBCOMB.pep:*

Pred. No. is the number of results predicted by chance to have a score greater than or equal to the score of the result being printed, and is derived by analysis of the total score distribution.

SUMMARIES

Result No.	Score	% Query		DB	ID	Description
		Match	Length			
1	2125	100.0	388	9	US-09-734-300-9	Sequence 9, Appli
2	2042	96.1	388	9	US-09-734-300-8	Sequence 8, Appli
3	1286.5	60.5	396	14	US-10-193-616-14	Sequence 14, Appl
4	1269	59.7	404	15	US-10-258-368-15	Sequence 15, Appl
5	1268	59.7	366	15	US-10-258-368-6	Sequence 6, Appli
6	1265	59.5	398	15	US-10-622-407-14	Sequence 14, Appl
7	1264.5	59.5	334	15	US-10-258-368-8	Sequence 8, Appli
8	1264.5	59.5	360	14	US-10-390-566-20	Sequence 20, Appl
9	1264.5	59.5	360	14	US-10-390-566-27	Sequence 27, Appl
10	1264.5	59.5	367	14	US-10-390-566-19	Sequence 19, Appl
11	1264.5	59.5	367	14	US-10-390-566-26	Sequence 26, Appl
12	1263.5	59.5	360	14	US-10-390-566-7	Sequence 7, Appli
13	1263.5	59.5	360	14	US-10-390-566-14	Sequence 14, Appl
14	1263.5	59.5	367	14	US-10-390-566-6	Sequence 6, Appli
15	1263.5	59.5	367	14	US-10-390-566-13	Sequence 13, Appl
16	1263	59.4	592	9	US-09-313-942-8	Sequence 8, Appli
17	1263	59.4	592	9	US-09-935-868-8	Sequence 8, Appli
18	1263	59.4	592	14	US-10-287-035-8	Sequence 8, Appli
19	1263	59.4	592	14	US-10-282-162-8	Sequence 8, Appli
20	1262.5	59.4	376	9	US-09-949-713-22	Sequence 22, Appl
21	1262.5	59.4	376	14	US-10-084-139-10	Sequence 10, Appl
22	1259	59.2	608	14	US-10-363-427-10	Sequence 10, Appl
23	1258	59.2	358	14	US-10-233-150-5	Sequence 5, Appli
24	1257.5	59.2	492	9	US-09-845-899A-3	Sequence 3, Appli
25	1257.5	59.2	492	17	US-10-473-127-1960	Sequence 1960, Ap
26	1257	59.2	360	9	US-09-949-713-11	Sequence 11, Appl
27	1257	59.2	776	9	US-09-935-868-36	Sequence 36, Appl
28	1257	59.2	776	9	US-09-935-868-40	Sequence 40, Appl
29	1257	59.2	776	9	US-09-935-868-44	Sequence 44, Appl
30	1256	59.1	397	9	US-09-854-864-18	Sequence 18, Appl
31	1256	59.1	397	9	US-09-855-158-18	Sequence 18, Appl
32	1254.5	59.0	367	15	US-10-452-646-9	Sequence 9, Appli
33	1254.5	59.0	1367	17	US-10-473-127-281	Sequence 281, App
34	1253.5	59.0	480	17	US-10-473-127-1964	Sequence 1964, Ap
35	1252.5	58.9	450	17	US-10-768-932A-2	Sequence 2, Appli
36	1252.5	58.9	784	9	US-09-313-942-30	Sequence 30, Appl
37	1252.5	58.9	784	9	US-09-935-868-30	Sequence 30, Appl
38	1252.5	58.9	784	14	US-10-287-035-30	Sequence 30, Appl
39	1252.5	58.9	784	14	US-10-282-162-30	Sequence 30, Appl
40	1252	58.9	388	9	US-09-784-623-16	Sequence 16, Appl
41	1252	58.9	388	17	US-10-748-112-3	Sequence 3, Appli
42	1251.5	58.9	347	9	US-09-796-033-8	Sequence 8, Appli
43	1251.5	58.9	347	9	US-09-730-465-8	Sequence 8, Appli
44	1251.5	58.9	347	13	US-10-091-236-17	Sequence 17, Appl
45	1251.5	58.9	347	14	US-10-091-313-7	Sequence 7, Appli